

Exhibit 3: Emboss Align (Nucleic Acid) Alignment

```
#####
# Program: needle
# Rndate: Fri Dec 21 19:40:04 2007
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20071221-19400372876934.output
#####
```

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#=====
#
# Aligned_sequences: 2
# 1: SEQ147
# 2: T_petrophila
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 939
# Identity:      890/939 (94.8%)
# Similarity:    890/939 (94.8%)
# Gaps:          3/939 ( 0.3%)
# Score: 5073.0
#
#
#=====
```

SEQ147	1	atgaacgatttgatcagaaagtacgctaaagatcaactggaaactttgaa	50
T_petrophila	1	atgaacgatttgatcagaaagtacgctaaagatcaactggaaattttgaa	50
SEQ147	51	aaggatcatagaaaagtctgaaggaatatccatcctcataaatggagaag	100
T_petrophila	51	aaggatcatagaaaagtctgaaggaatatccattctcataaacggagaag	100
SEQ147	101	atctctcgtatccgagagaagtatcccttgaacttcccaggtacgtggag	150
T_petrophila	101	atctctcgtatccgagagaagtatcccttgaacttcccaggtacgtggag	150
SEQ147	151	aaatttccccgaaggcctcggatgttctggagatagatcccaggggga	200
T_petrophila	151	aaatttccccgaaggcctcggatgttctggaggtagatcccagggagga	200
SEQ147	201	gaacataggcatagacgacatcagaacgataaaggacttcctgaactaca	250
T_petrophila	201	gaacatagggtatagacgaaatcagaacgataaaggacttcctgaactaca	250
SEQ147	251	gccccgagctctacacgagaaagtacgtgatagtcacgactgtgaaaga	300
T_petrophila	251	gccctgaactctacacgagaaagtacgtgatagtcacgactgtgaaaga	300
SEQ147	301	atgacccagcaggcggcgaaacgcgtttctgaaggcccttgaagaaccacc	350
T_petrophila	301	atgacccagcaggcggcgaaacgcgtttctgaaaacccttgaagaaccgcc	350
SEQ147	351	agaatacgctgtgatcggttctgaacactcgccgctggcattatctactgc	400
T_petrophila	351	agaatacgctgtgatcggttctgaacacccgccactggcattatctactgc	400

SEQ147	401	cgacgataaagagccgagtggttcagagtggttggaacggtccaaaggag	450
T_petrophila	401	cgacgataaagagccgagtggttcagagtggttggaacggtccaaaggag	450
SEQ147	451	ttcagagatctcgtgaaagagaaaataggagatctctgggaggaacttcc	500
T_petrophila	451	ttcagagatctcgtgaaagagaaaataggcgatctctgggaggaacttcc	500
SEQ147	501	acttcttgagagagacttcaaaacggctctcgaagcctacaaacttggtg	550
		. .	
T_petrophila	501	gctccttgagagagacttcaaaacggcttctcgaagcctacaaacttggtg	550
SEQ147	551	cggaaaaactttctggattgatggaaagtctcaaagttttggagacggaa	600
T_petrophila	551	cggaaaaactttctggattgatggaaagtctcaaagttttggagacggaa	600
SEQ147	601	aaactcttgaaaaaggctctttcaaaaggcctcgaagggttatctcgcatg	650
		
T_petrophila	601	aaactcttaaaagaaagccctttcagaaggactcgagggttatctcgcggtg	650
SEQ147	651	tagggagctcctggagagattttcaaagggtggaatcgaaggaattctttg	700
		.	
T_petrophila	651	tagggagcttctggagagattttcaaagggtggaatcgaaggaattctttg	700
SEQ147	701	cgctttttgatcaggtgactaacacgataaacaggaaaagacgcgtttctt	750
		
T_petrophila	701	cgctttttgaccaattaaccaacacgataaacgggaaaagactcatttctt	750
SEQ147	751	ttgatccagagactgacaagaatcattctccacgaaaacacatgggaaag	800
		
T_petrophila	751	ttgatccagagactgacaagaattgtccttcacgaaaacacctgggaaag	800
SEQ147	801	cgttgaagatcaaaaaagcgtgtctttcctcgattcaattctcaggggtga	850
T_petrophila	801	cgttgaagatcaaaaaagcgtgtctttcctcgattcaattctcaggggtga	850
SEQ147	851	agatagcgaatctgaacaacaaactcactctgatgaacatcctcgcgata	900
		.	
T_petrophila	851	aaatagcgaatctgaacaacaaactcactctgatgaatattctcgcgata	900
SEQ147	901	cacagagagagaaagagaggtgtcaacgcttggagc	936
T_petrophila	901	cacagagagagaaagagaggtgtcaacgcttggagctga	939